In the Specification:

Please amend the specification as shown:

Please insert the following on page 1, after the title:

SEQUENCE LISTING

The instant application contains a Sequence Listing which has been submitted via EFS-Web and is hereby incorporated by reference in its entirety. Said ASCII copy, created on July 16, 2010, is named WEICKM58.txt and is 4,401 bytes in size.

Please delete the paragraph on page 8, line 33 to page 9, line 11 and replace it with the following paragraph:

As used herein, the term "neurturin product" includes neurturin protein products such as purified natural or synthetic neurturin and variants thereof. Variants include insertion, substitution and deletion variants and chemically modified derivatives. Variants also include recombinant proteins, for example but not limited to hybrids of neurturin and other TGF-beta proteins (preferably from the GDNF-family). Also included are proteins or peptides substantially homologous to the human neurturin precursor protein having the amino acid sequence published as GenBank Accession Number NP_004549 **(SEQ ID NO: 7 and the corresponding coding nucleotide sequence from GenBank Accession Number U78110 disclosed as SEQ ID NO: 6)**. The term "neurturin product" also includes polynucleotides (e.g. mRNA/DNA) encoding the above described neurturin protein product. The term “neurturin product” also includes neurturin homodimers or heterodimers of a neurturin protein product and another protein, wherein the other protein preferably belongs to the GDNF-family.

Please delete the paragraph on page 9, line 20 to page 10, line 11 and replace it with the following paragraph:

The term "substantially homologous" as used herein means having a degree of homology to the biologically active human neurturin product resulting from the cleavage of the neurturin precursor having the amino acid sequence published as GenBank Accession Number NP_004549 **(SEQ ID NO: 7 and the corresponding coding nucleotide sequence from GenBank Accession Number U78110 disclosed as SEQ ID NO: 6)** or to the human neuturin precursor itself, that is preferably in excess of 70%, most preferably in excess of 80%, and even more preferably in excess of 90% or 95%. The degree of homology between the mouse and the human protein is about 91 %, and it is contemplated that preferred mammalian neurturin proteins will have a

similarly high degree of homology. Also included are proteins which are hybrids between neurturin and another TGFbeta-protein, preferably another member of the GDNF-family which retain the stimulatory effect on islet cell formation found in Neurturin. The percentage of homology or identity between a neurturin product and the human neurturin protein or a precursor or a nucleic acid coding therefor may be determined according to standard procedures, e.g. by using the BLAST algorithm. Preferably, the percentage of homology or identity is calculated as the percentage of nucleotide or amino acid residues found in the smaller of the two sequences that align with identical nucleotides or amino acid residues in the sequence being compared, when four gaps in a length of 100 nucleotides or amino acids may be introduced to assist in that alignment. Also included as substantially homologous is any neurturin protein product which may be isolated by virtue of cross-reactivity with antibodies to the neurturin protein product or whose genes may be isolated through hybridization with the gene or with segments of the gene encoding the neurturin protein product.

Please delete the paragraph on page 30, line 18 to page 31, line 1 and replace it with the following paragraph:

Expression levels of pancreas specific genes was measured by semi-quantitative RT-PCR analysis. Differentiated wild type ES and Pax4 ES cells were collected after embryoid body formation and suspended in lysis buffer (4 M guanidinium thiocyanate, 25 mM sodium citrate, pH 7; 0.5% sarcosyl, 0.1 M beta-mercaptoethanol). Total RNA was isolated by the single step extraction method described by Chomczynski & Sacchi, 1987, Anal. Biochem. 162: 156-159). mRNA was reverse transcribed using PolyT tail primer Oligo $d(T)_{16}$ (PerkinElmer) **(SEQ ID NO: 8)** and the resulting cDNA was amplified using oligonucleotide primers complementary and identical to transcripts of beta-cell glucose transporter Glut2 and insulin. The house keeping gene beta-tubulin was used as internal standard. Reverse transcription (RT) was performed with MuLV reverse transcriptase (Perkin Elmer). Multiplex PCRs were carried out using AmpliTaq DNA polymerase (Perkin Elmer) as described in Wobus at al., 1997, supra. mRNA levels of genes encoding Glut2 and insulin were analysed using the Dynalbeads mRNA DIRECT micro kit (Dynal) according to the manufacturer's instructions.

Please delete the paragraphs on page 36, lines 6-27 and replace them with the following paragraphs:

Example 9: Genotype analysis of rIP-*mDG770* transgenic mice

Genotyping was performed by PCR using genomic DNA isolated from the tail tip. To detect the *mDG770* transgene a transgene specific forward primer (5` tgc tat ctg tct gga tgt gcc 3` **(SEQ ID NO: 1)** and a *mDG770* transgene specific reverse primer (5` aag gac acc tcg tcc tca tag 3` **(SEQ ID NO: 2)**) was used.

Example 10: *mDG770* expression analysis via TaqMan analysis

The expression of the *mDG770* transgene in islets was monitored by TaqMan analysis. For this analysis, 25 ng cDNA derived from pancreatic islet RNA isolated from transgenic mice and their littermates and a *mDG770* specifc primer/probe pair were used to detect endogenous as well as transgenic *mDG770* expression (*mDG770-1* forward primer: 5` GCC TAT GAG GAC GAG GTG TCC 3` **(SEQ ID NO: 3)**, *mDG770* reverse primer: 5` AGC TCT TGC AGC GTG TGG T 3` **(SEQ ID NO: 4)**, *mDG770* probe: 5' TCC TGG ACG TGC ACA GCC GC 3' **(SEQ ID NO: 5)**). TaqMan analysis was performed using standard techniques known to those skilled in the art. Ectopic transgene expression was detected in 3 of 4 rIP-*mDG770* transgenic founderlines analysed. The two founderlines showing highest transgene expression levels were used for further analysis. For the level of mDG70 expression in islets of a transgenic animal compared to a wild-type animal, see also Fig. 3.